

Sequence of a cDNA coding for human IRF-2

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We have previously isolated a cDNA clone, a mouse interferon regulatory factor-2 (IRF-2) (Harada, H., Fujita, T., Miyamoto, M., Kimura, Y., Maruyama, M., Furia, A., Miyata, T. and Taniguchi, T., 1989, *Cell*, 58, 729-739). We have isolated a human IRF-2 cDNA coding for human IRF-2 by cross-hybridization with the mouse IRF-2 full length cDNA probe, using the human T cell line, Jurkat-111 cDNA library.

One of the positive clones, pHIRF4S-51, was sequenced. This cDNA includes 98 bp of 5'-untranslated, 1047 bp of coding and 999 bp of 3'-untranslated regions. The deduced amino acid sequence is the 349 amino acid protein and this protein shows 93.5% homology, compared with mouse IRF-2. Furthermore, the amino terminal half of human IRF-2 from 1 to 113 amino acid has 73% homology to human IRF-1 (Maruyama, M., Fujita, T. and Taniguchi, T., *Nucleic Acids Research*, 1989, 7, 3292).

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1  AACTGACGGGCTTTCATTCCATTTCCACACCCTAGCAACACTTATACCTTGCAGGAAATGTATTGGTAGCGTGAAAAAGCACACTGAGAGGGCACC
99  ATG CCG GTG GAA AGG ATG CCG ATG CCG CCG TGG CTG GAG GAG CAG ATA AAC TCC AAC ACG ATC CCG GGG CTC AAG
    Met Pro Val Glu Arg Met Arg Met Arg Pro Trp Leu Glu Glu Glu Gln Ile Asn Ser Asn Thr Ile Pro Gly Leu Lys
174  TGG CTT AAC AAG GAA AAG AAG ATT TTT CAG ATC CCC TGG ATG CAT GCG GCT AGA CAT GGG TGG GAT GTG GAA AAA
    Trp Leu Asn Lys Glu Lys Lys Ile Phe Gln Ile Pro Trp Met His Ala Ala Arg His Gly Trp Asp Val Glu Lys
249  GAT GCA CCA CTC TTT AGA AAC CCG GCA ATC CAT ACA GGA AAG CAT CAA CCA GGA GTA GAT AAA CCT GAT CCC AAA
    Asp Ala Pro Leu Phe Arg Asn Arg Ala Ile His Thr Gly Lys His Gln Pro Gly Val Asp Lys Pro Asp Pro Lys
324  ACA TGG AAG GCG AAT TTC AGA TGC GCC ATG AAT TCC TTG CCT GAT ATT GAA GAA GTC AAG GAT AAA AGC ATA AAG
    Thr Trp Lys Ala Asn Phe Arg Cys Ala Met Asn Ser Leu Pro Asp Ile Glu Glu Val Lys Asp Lys Ser Ile Lys
399  AAA GGA AAT AAT GCC TTC AGG GTC TAC CGA ATG CTG CCC CTA TCA GAA CCG CCT TCT AAG AAA GGA AAG AAA CCA
    Lys Gly Asn Asn Ala Phe Arg Val Tyr Arg Met Leu Pro Leu Ser Glu Arg Pro Ser Lys Lys Gly Lys Lys Pro
474  AAG ACA GAA AAA GAA GAC AAA GTT AAG CAC ATC AAG CAA GAA CCA GTT GAG TCA TCT CTG GGG CTT AGT AAT GGA
    Lys Thr Glu Lys Glu Asp Lys Val Lys His Ile Lys Gln Glu Pro Val Glu Ser Ser Leu Gly Leu Ser Asn Gly
549  GTA AGT GAT CTT TCT CCT GAG TAT GCG GTC CTG ACT TCA ACT ATA AAA AAT GAA GTG GAT AGT ACG GTG AAC ATC
    Val Ser Asp Ile Ser Pro Glu Tyr Ala Val Leu Thr Ser Thr Thr Ile Lys Asn Glu Val Asp Ser Thr Val Asn Ile
624  ATA GTT GTA GGA CAG TCC CAT CTG GAC AGC AAC ATT GAG AAT CAA GAG ATT GTC ACC AAT CCG CCA GAC ATT TGC
    Ile Val Val Gly Gln Ser His Leu Asp Ser Asn Ile Glu Asn Gln Glu Ile Val Thr Asn Pro Asp Ser Ile Cys
699  CAA GTT GTA GAG GTC ACC ACT GAG AGC GAC GAG CAG CCG GTC AGC ATG AGC GAG CTC TCC CCT CTG CAG CAT TCC
    Gln Val Val Glu Val Thr Thr Glu Ser Asp Glu Gln Pro Val Ser Met Ser Glu Leu Tyr Pro Leu Gln Ile Ser
774  CCC GTG TCT TCC TAT GCA GAA AGC GAA ACG ACT GAT AGT GTG CCC AGC ATG GAA GAG AGT GCC GAG GGG CGG CCA
    Pro Val Ser Ser Tyr Ala Glu Ser Glu Thr Thr Asp Ser Val Pro Ser Asp Glu Glu Ser Ala Glu Gly Arg Pro
849  CAC TGG CCG AAG AGG AAT ATT GAA GGC AAA CAG TAC CTC AGC AAC ATG GGG ACT CGA GGC TCC TAC CTG CTG CCC
    His Trp Arg Lys Arg Asn Ile Glu Gly Lys Gln Tyr Leu Ser Asn Met Gly Thr Arg Gly Ser Tyr Leu Leu Pro
924  GGC ATG GCG TCC TTC CTG ACT TCC AAC AAA CCG GAC CTC CAG GTC ACC ATC AAA GCG GAG AGC AAT CCG GTG CCT
    Gly Met Ala Ser Phe Val Thr Ser Asn Lys Pro Asp Leu Gln Val Thr Ile Lys Glu Glu Ser Asn Pro Val Pro
999  TAC AAC AGC TCC TGG CCC CCT TTT CAA GAC CTC CCC CTT TCT TCC TCC ATG ACC CCA GCA TCC AGC AGC AGT CCG
    Tyr Asn Ser Ser Trp Pro Pro Phe Gln Asp Leu Thr Leu Ser Ser Ser Ser Thr Pro Ala Ser Ser Ser Arg
1074 CCA GAC CCG GAG ACC CCG GCC AGC GTC ATC AAG AAA ACA TCG GAT ATC ACC GAG ACC CCG GTC AAG AGC TGT TAA
    Pro Asp Arg Glu Thr Ser Thr Arg Ala Ser Val Ile Lys Lys Thr Ser Asp Thr Thr Gln Ala Arg Val Lys Ser Cys ***
1149 GCCTGACTCTCCGCGGTGGTGTGGGGCTTCTGGCTTGTGGTTGTGGTTGTGGTATTTGTTTTTCTCTGACACCTATTTAGACAAAT
1248 CTAAAGGGAAAAAGCCTTGACATAGAACAATTGATTCGTGTGTCCAACCTCCAGTACCTGGAGCTCTCTCTTAACTCAGGACTCCAGCCCATGGTAGACG
1347 TGTGTTCTAGAGCCTGCTGGATCTCCCAAGGGCTACTCACTCAAGTTCGAAGGACCAACCAAGGGCAGTGGAGGTTGCTGCATGGCTGGCGTCAAGGCCAG
1446 CAAGGTGGAGTGGATGCCCTCAGAACCGGACGATATGTGAAGTACTAGCTGGAATTTTTTATCTTGTTGAATATGACATAGGCAGCAGCTAGGCACATTCG
1545 AGCTGCTCTGACACCTTATCTTAAAGCACTTACAGATAGCCCTCTTTGTGATCTTGCCTATCTCACAACGAGCAGCTCAGCAGCCCTTCTCTGCCATTC
1644 CCCCAGCCCTCTCTTCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCCCATCC
1743 ATCCGGAGGAGGAAAGGAAATGAAATTTCTCTACAGATGCCATTTTCAGACTGCTTTAAAAAAAATCCTTCTAATTCGTATGCTTGGTAAATGCCACG
1842 GGTACAAAAGGAAAGTATCATGGAAATATATGCCAAATCCAGCAATTTGAAGACAAAAATACTCTAACTTCAACAGGACGAAGCTTTTTATTTTTTA
1941 TACAGGGGAATTTTTTAAAGTAAAAATCAAAATAAAAATAAATGTTTTTATCTTTCTACACGAAATTTATAATTTTAAGATTCCTTCTCTG
2040 TTTATCAGCAGTGTATTACCATCTTGTGGCACAATTTTTTTAAATTTTGAAGGTAAGAAAAGCTTTTATGAGCTCATCTAGCAATCAGATTTTCC
2139 TGTGGA
    
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